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SEP 16 2003

TECH CENTER 1600/2900

1600

RAW SEQUENCE LISTING

DATE: 09/12/2003

PATENT APPLICATION: US/09/077,572

TIME: 12:58:04

Input Set : A:\09-077572 Sequence Listing.txt

Output Set: N:\CRF4\09122003\I077572.raw

4 <110> APPLICANT: Apicella, M.A.
5 Sunshine, M.G.
6 Lee, N.
7 Gibson, B.
8 Arumugham, R.
10 <120> TITLE OF INVENTION: Non-toxic mutants of pathogenic gram-negative bacteria
12 <130> FILE REFERENCE: 875.001US2
14 <140> CURRENT APPLICATION NUMBER: US 09/077,572
15 <141> CURRENT FILING DATE: 1998-10-13
17 <150> PRIOR APPLICATION NUMBER: PCT/US96/18984
18 <151> PRIOR FILING DATE: 1996-11-27
20 <150> PRIOR APPLICATION NUMBER: US 08/565,943
21 <151> PRIOR FILING DATE: 1995-12-01
23 <160> NUMBER OF SEQ ID NOS: 5
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 969
29 <212> TYPE: DNA
30 <213> ORGANISM: Haemophilus influenzae, strain 2019
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (34)...(966)
36 <400> SEQUENCE: 1

37	taaactacgc ccctaactta cgtggaaaga aca atg aaa aac gaa aaa ctc cct	54
38	Met Lys Asn Glu Lys Leu Pro	
39	1 5	
41	caa ttt caa ccg cac ttt tta gcc cca aaa tac tgg ctt ttt tgg cta	102
42	Gln Phe Gln Pro His Phe Leu Ala Pro Lys Tyr Trp Leu Phe Trp Leu	
43	10 15 20	
45	ggc gtg gca att tgg cga agt att tta tgt ctt ccc tat cct att ttg	150
46	Gly Val Ala Ile Trp Arg Ser Ile Leu Cys Leu Pro Tyr Pro Ile Leu	
47	25 30 35	
49	cgc cat att ggt cat ggt ttc ggt tgg ctg ttt tca cat tta aaa gtg	198
50	Arg His Ile Gly His Gly Phe Gly Trp Leu Phe Ser His Leu Lys Val	
51	40 45 50 55	
53	ggt aaa cgt cga gct gcc att gca cgc cgt aat ctt gaa ctt tgt ttc	246
54	Gly Lys Arg Arg Ala Ala Ile Ala Arg Arg Asn Leu Glu Leu Cys Phe	
55	60 65 70	
57	cct gat atg cct gaa aac gaa cgt gag acg att ttg caa gaa aat ctt	294
58	Pro Asp Met Pro Glu Asn Glu Arg Glu Thr Ile Leu Gln Glu Asn Leu	
59	75 80 85	
61	cgt tca gta ggc atg gca att atc gaa act ggc atg gct tgg ttt tgg	342
62	Arg Ser Val Gly Met Ala Ile Ile Glu Thr Gly Met Ala Trp Phe Trp	

ENTERED

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63	90	95	100	
65	tcg gat tca cgt atc aaa aaa tgg tcg aaa gtt gaa ggc tta cat tat	390		
66	Ser Asp Ser Arg Ile Lys Lys Trp Ser Lys Val Glu Gly Leu His Tyr			
67	105 110 115			
69	cta aaa gaa aat caa aaa gat gga att gtt ctc gtc ggc gtt cat ttc	438		
70	Leu Lys Glu Asn Gln Lys Asp Gly Ile Val Leu Val Gly Val His Phe			
71	120 125 130 135			
73	tta acg cta gaa ctt ggc gca cgc atc att ggt tta cat cat cct ggc	486		
74	Leu Thr Leu Glu Leu Gly Ala Arg Ile Ile Gly Leu His His Pro Gly			
75	140 145 150			
77	att ggt gtt tat cgt cca aat gat aat cct ttg ctt gat tgg cta caa	534		
78	Ile Gly Val Tyr Arg Pro Asn Asp Asn Pro Leu Leu Asp Trp Leu Gln			
79	155 160 165			
81	aca caa ggc cgt tta cgc tcc aat aaa gat atg ctt gat cgt aaa gat	582		
82	Thr Gln Gly Arg Leu Arg Ser Asn Lys Asp Met Leu Asp Arg Lys Asp			
83	170 175 180			
85	tta cgc gga atg atc aaa gct tta cgc cac gaa gaa acc att tgg tat	630		
86	Leu Arg Gly Met Ile Lys Ala Leu Arg His Glu Glu Thr Ile Trp Tyr			
87	185 190 195			
89	gcg cct gat cac gat tac ggc aga aaa aat gcc gtt ttt gtt cct ttt	678		
90	Ala Pro Asp His Asp Tyr Gly Arg Lys Asn Ala Val Phe Val Pro Phe			
91	200 205 210 215			
93	ttt gca gta cct gac act tgc act act act ggt agt tat tat tta ttg	726		
94	Phe Ala Val Pro Asp Thr Cys Thr Thr Thr Gly Ser Tyr Tyr Leu Leu			
95	220 225 230			
97	aaa tcc tcg caa aac agc aaa gtg att cca ttt gcg cca tta cgc aat	774		
98	Lys Ser Ser Gln Asn Ser Lys Val Ile Pro Phe Ala Pro Leu Arg Asn			
99	235 240 245			
101	aaa gat ggt tca ggc tat acc gtg agc att tca gcg cct gtt gat ttt	822		
102	Lys Asp Gly Ser Gly Tyr Thr Val Ser Ile Ser Ala Pro Val Asp Phe			
103	250 255 260			
105	aca gat tta caa gat gaa gta gcg ata gct gtg cga atg aat caa atc	870		
106	Thr Asp Leu Gln Asp Glu Val Ala Ile Ala Val Arg Met Asn Gln Ile			
107	265 270 275			
109	gtt gaa aag gaa atc atg aag ggc ata tca caa tat atg tgg cta cat	918		
110	Val Glu Lys Glu Ile Met Lys Gly Ile Ser Gln Tyr Met Trp Leu His			
111	280 285 290 295			
113	cgt cgt ttt aaa aca cgc ccc gat gaa aat acg cct agt tta tac gat	966		
114	Arg Arg Phe Lys Thr Arg Pro Asp Glu Asn Thr Pro Ser Leu Tyr Asp			
115	300 305 310			
117	taa	969		
119	<210> SEQ ID NO: 2			
120	<211> LENGTH: 31			
121	<212> TYPE: DNA			
122	<213> ORGANISM: Haemophilus influenzae, strain 2019			
124	<400> SEQUENCE: 2			
125	ccaatatggc gcaaaatagg atagggaaga c	31		
127	<210> SEQ ID NO: 3			
128	<211> LENGTH: 9			

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Input Set : A:\09-077572 Sequence Listing.txt

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129 <212> TYPE: DNA
130 <213> ORGANISM: Unknown
132 <220> FEATURE:
133 <223> OTHER INFORMATION: An uptake sequence involved in a transformation
134 process for H. influenzae.
136 <400> SEQUENCE: 3
137 aagtgcggt 9
139 <210> SEQ ID NO: 4
140 <211> LENGTH: 30
141 <212> TYPE: DNA
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 4
145 atctctcagc tccacgccat tggccaggag 30
147 <210> SEQ ID NO: 5
148 <211> LENGTH: 30
149 <212> TYPE: DNA
150 <213> ORGANISM: Homo sapiens
152 <400> SEQUENCE: 5
153 ctcttgcca atggcgtgga gctgagagat 30

VERIFICATION SUMMARY

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